

OM protein - protein search, using sw model

Run on: March 14, 2001, 16:12:15 ; Search time 14.09 seconds
(without alignments)
578.602 Million cell updates/sec

Title: US-09-455-486-6

Perfect score: 2351

Sequence: 1 MESISMWSPKSLSETCLPN.....ALVLPISIVLDLQLCRYPD 454

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Min DB seq length: 0

Max DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA.*

- 1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/6.COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	31.3	141	3	US-09-083-521-1
2	107.5	4.6	695	1	Sequence 1, Appli
3	107.5	4.6	695	3	Sequence 2, Appli
4	99	4.2	531	2	Sequence 2, Appli
5	97.5	4.1	390	3	Sequence 2, Appli
6	93	4.0	365	2	Sequence 3, Appli
7	89.5	3.8	495	1	Sequence 2, Appli
8	89.5	3.8	495	1	Sequence 2, Appli
9	89.5	3.8	495	2	Sequence 2, Appli
10	89.5	3.8	495	2	Sequence 2, Appli
11	89.5	3.8	495	2	Sequence 2, Appli
12	89	3.8	1582	2	Sequence 9, Appli
13	89	3.8	1582	3	Sequence 9, Appli
14	89	3.8	1582	3	Sequence 9, Appli
15	88.5	3.8	591	1	Sequence 2, Appli
16	88.5	3.8	591	1	Sequence 2, Appli
17	87	3.7	457	2	Sequence 3, Appli
18	86.5	3.7	699	1	Sequence 7, Appli
19	86.5	3.7	699	2	Sequence 7, Appli
20	85.5	3.6	861	3	Sequence 2, Appli
21	85	3.6	1581	2	Sequence 6, Appli
22	85	3.6	1581	3	Sequence 6, Appli
23	85	3.6	1581	3	Sequence 6, Appli
24	84.5	3.6	550	1	Sequence 4, Appli
25	84.5	3.6	550	2	Sequence 4, Appli
26	84.5	3.6	550	2	Sequence 4, Appli
27	84.5	3.6	550	4	Sequence 4, Appli
28	84	3.6	323	2	Sequence 2, Appli

Sequence 2, Appli
Sequence 9, Appli
Sequence 14, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 20, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-083-521-1
; Sequence 1, Application US/09083521
; Patent No. 6048970
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,521
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0527 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT10
; CLONE: 1691243
; US-09-083-521-1

102(e) = 05/22/98

Query Match 31.3%; Score 736; DB 3; Length 141;

Best Local Similarity 100.0%; Pred. No. 5.9e-70;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 MVHVSILCLPMSRSRYFLFNMAVQOVHANISNWEDEEVRIEYISFGINSGLSL 373

Db 1 MHVAYSLCLPMRRSRYFLNMAVQOVHANIENSNNEEVEVRIEMXISFGINSGLLSL 60
 QY 374 LAVTSIPSVSNALNWRPESFIQSTGYVALLISTFVLVLYGKRAPEEYRYFTPTPNFV 433
 Db 61 LAVTSIPSVSNALNWRPESFIQSTGYVALLISTFVLVLYGKRAPEEYRYFTPTPNFV 120
 QY 434 LALVLPSTVILDLQLCRYPD 454
 Db 121 LALVLPSTVILDLQLCRYPD 141
 RESULT 2
 US-08-487-886-2
 Sequence 2, Application US/08487886
 Patent No. 5744448
 GENERAL INFORMATION:
 APPLICANT: Kelton, Christie Ann
 APPLICANT: Schweickhardt, Rene Lynn
 APPLICANT: Cheng, Shirley Vul Yen
 APPLICANT: Nugent, No. 574448een Patrice
 TITLE OF INVENTION: Human Follicle Stimulating
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephan P. Williams,
 ADDRESSEE: Ares-Serono, Inc.
 STREET: Exchange Place, 37th floor
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
 COMPUTER: IBM PS/2, model 55 SX
 OPERATING SYSTEM: MS-DOS version 4.0
 SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487.886
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/670.085
 FILING DATE: 15-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Stephan P.
 REGISTRATION NUMBER: 28546
 REFERENCE/DOCKET NUMBER: US/252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 723-1300
 TELEFAX: (617) 723-8923
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 695
 TYPE: Amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -17 to -1
 IDENTIFICATION METHOD: hydrophobic
 FEATURE:
 NAME/KEY: putative amino-terminal 'extracellular domain
 LOCATION: 1 to 349
 IDENTIFICATION METHOD: similarity with other
 IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
 IDENTIFICATION METHOD: domains, hydrophilic
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 350 to 613
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains
 FEATURE:
 NAME/KEY: putative transmembrane region I

LOCATION: 350 to 370
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region II
 LOCATION: 382 to 404
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region III
 LOCATION: 427 to 448
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region IV
 LOCATION: 469 to 491
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region V
 LOCATION: 512 to 533
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region VI
 LOCATION: 557 to 580
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative transmembrane region VII
 LOCATION: 592 to 613
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
 FEATURE:
 NAME/KEY: putative carboxy-terminal intracellular
 NAME/KEY: domain
 LOCATION: 614 to 678
 US-08-487-886-2

Query Match 4.6%; Score 107.5; DB 1: Length 695;
 Best Local Similarity 17.0%; Pred. No. 0.01;
 Matches 84; Conservative 77; Mismatches 146; Indels 185; Gaps 17;
 QY 79 HEDALTGTNLIFFVALHREHYTSLMDLRHLVLC-----KILIDVSNMR 121
 Db HEIRIEKANNL--LYINPEAFQNLPLNLOVLLISNTGKHLDPVHKIHSQKVLDDIODIN 156
 QY 122 INQYPSNAEYLASLFPDPSLIVKGVVYSAMALQGLPGDASQVYCSNNIQARQOVIEL 181
 Db 157 IH-----TIERNSEFVGLSFESVILWL-----NANGIOEIRNCA----- 189
 QY 182 AQQLNFIPIDGLSSSAREIENLRLFTLWKGPFVVVAISLATFFFLXSFVRDVIHPYAR 241
 Db 190 ---FNGTQIDELNLSDDNNLELPNDVFGASGVPVILDSIRIHSLSYGLNKKLRA 246
 QY 242 NOOSDFYKIPFIENKTL-PIVAITLLSLVY----- 271
 Db 247 RSTYLRKLP-----TLEKLVAMEASLTPSHCCAFANWRQRQISELHPICNKSILROE 300
 QY 272 -----LAGLLAAAYOLVYGYKRRF-----PWLETWLCRQOL 305
 Db 301 VDYMTQTRGORSLLAEDNESSYRGFDYTFEDVLCNEVVVDVTCSPKPAFNECDIM 360
 QY 306 G-----LLSFFFAVHVA-----YSICLPMRSSERYLFLNNAVQOVHANIE 347